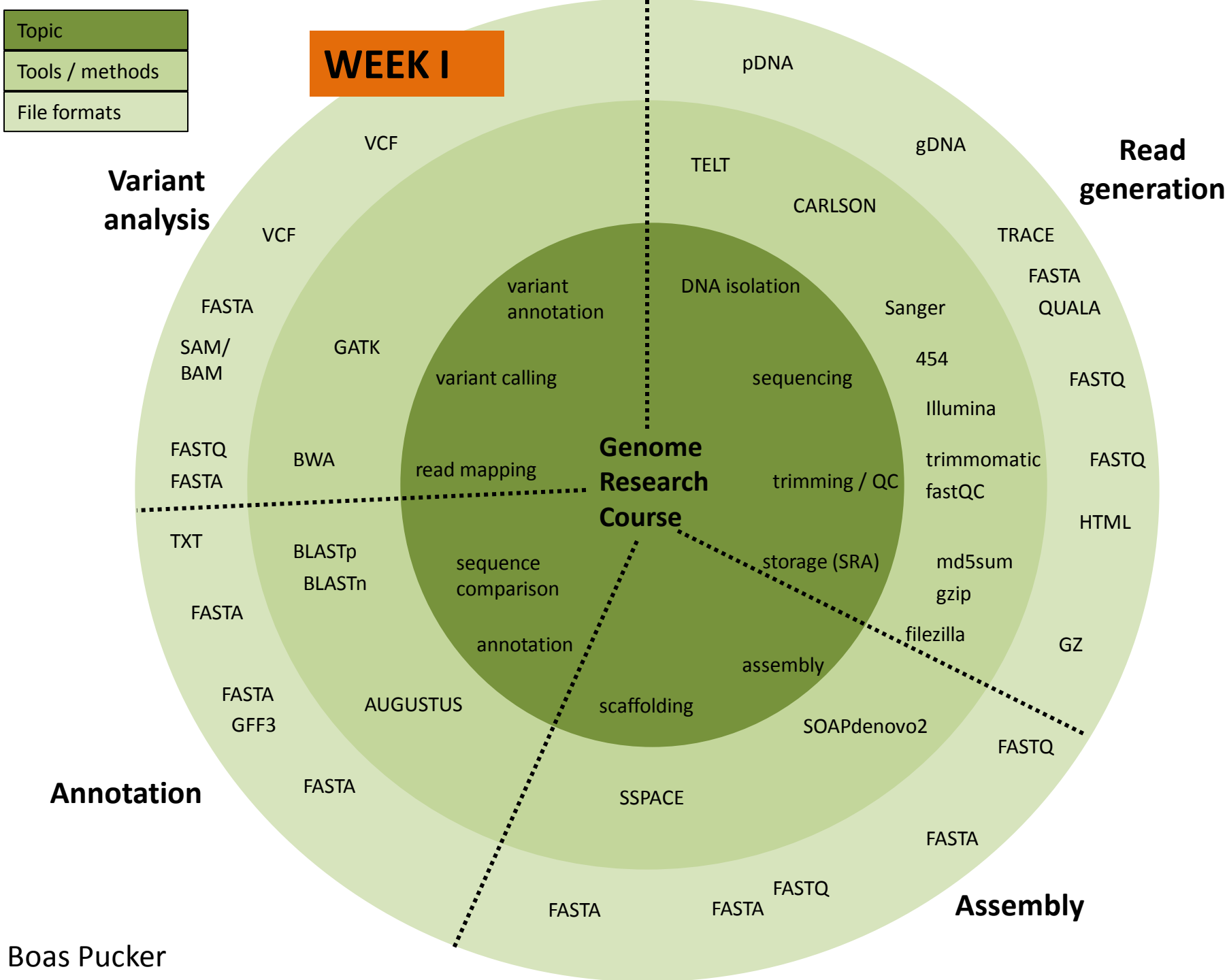
Topic
Tools / methods
File formats
WEEK I
Genome Research Course
Read generation
pDNA
gDNA
TELT
CARLSON
TRACE
FASTA
QUALA
FASTQ
FASTQ
HTML
DNA isolation
Sanger
454
Illumina
sequencing
trimmomatic
fastQC
trimming / QC
storage (SRA)
md5sum
gzip
filezilla
GZ
Assembly
FASTQ
FASTA
FASTQ
FASTA
FASTA
assembly
SOAPdenovo2
SSPACE
scaffolding
Annotation
FASTA
GFF3
FASTA
AUGUSTUS
annotation
sequence comparison
TXT
BLASTp
BLASTn
FASTA
read mapping
FASTQ
FASTA
BWA
Variant analysis
VCF
VCF
FASTA
SAM/ BAM
GATK
variant calling
variant annotation

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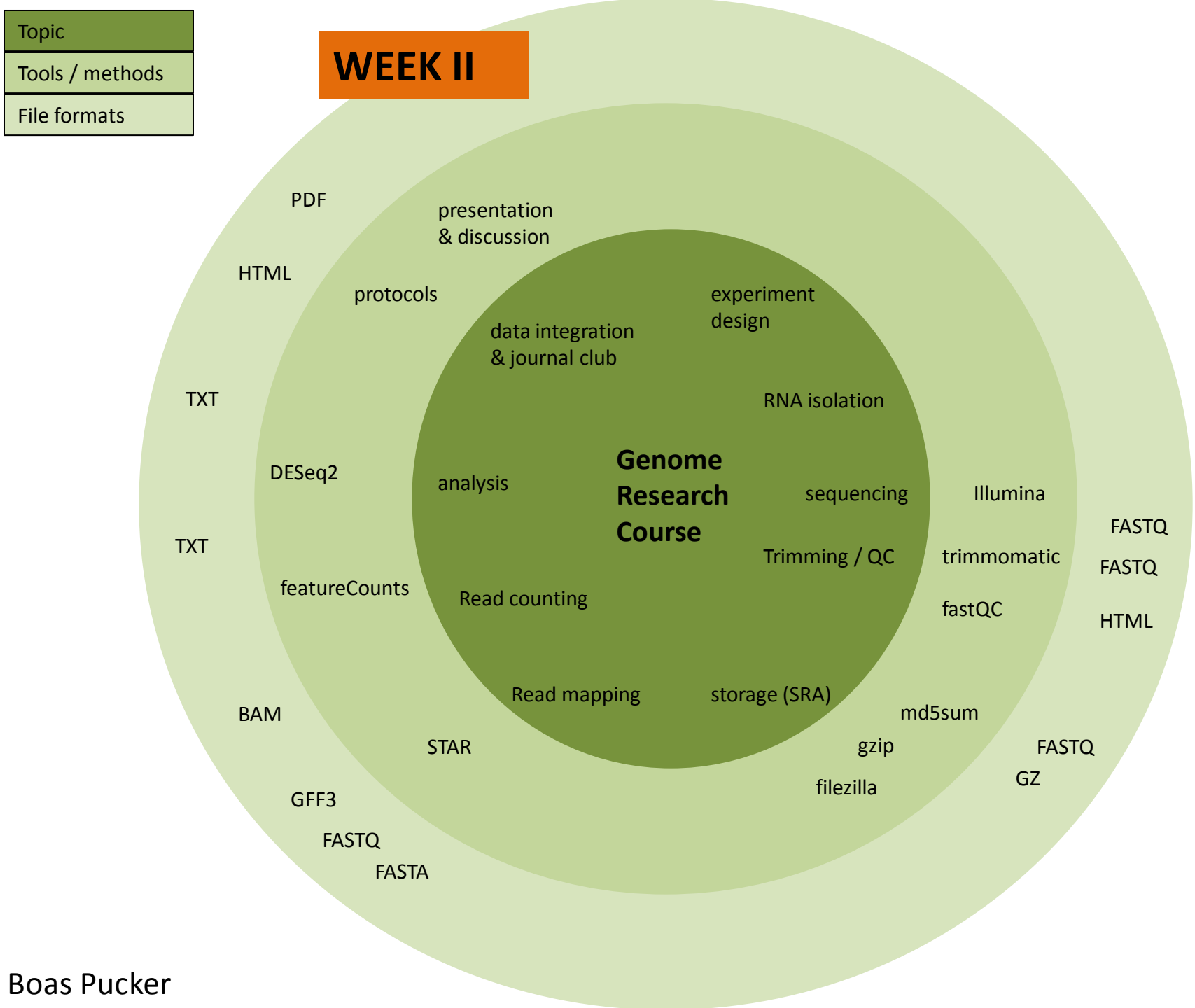
Topic
Tools / methods
File formats
WEEK II
Genome Research Course
PDF
presentation & discussion
HTML
protocols
experiment design
data integration & journal club
TXT
RNA isolation
DESeq2
analysis
sequencing
Illumina
FASTQ
TXT
Trimming / QC
trimmomatic
FASTQ
featureCounts
Read counting
fastQC
HTML
Read mapping
storage (SRA)
BAM
md5sum
STAR
gzip
FASTQ
GZ
filezilla
GFF3
FASTQ
FASTA

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